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RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/017,910

TIME: 15:47:43

Input Set : N:\Crf3\RULE60\10017910.txt

Output Set: N:\CRF3\02152002\J017910.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Choi, Yongwon

7 Wong, Brian

8 Josien, Regis

9 Steinman, Ralph

11 (ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY

12 INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING

SAME, AND

13 METHODS OF USE THEREOF

15 (iii) NUMBER OF SEQUENCES: 14

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Klauber & Jackson

19 (B) STREET: 411 Hackensack Avenue, 4th Floor

20 (C) CITY: Hackensack

21 (D) STATE: New Jersey

22 (E) COUNTRY: USA

23 (F) ZIP: 07601

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/10/017,910

C--> 33 (B) FILING DATE: 14-Dec-2001

39 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US 09/447,035

38 (B) FILING DATE: 1999-11-22

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Jackson Esq., David A.

43 (B) REGISTRATION NUMBER: 26,742

44 (C) REFERENCE/DOCKET NUMBER: 600-1-200

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: 201-487-5800

48 (B) TELEFAX: 201-343-1684

49 (C) TELEX: 133521

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1823 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: double

58 (D) TOPOLOGY: linear

ENTERED

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60      (ii) MOLECULE TYPE: cDNA
62      (iii) HYPOTHETICAL: NO
64      (vi) ORIGINAL SOURCE:
65          (A) ORGANISM: Homo sapiens
67      (ix) FEATURE:
68          (A) NAME/KEY: CDS
69          (B) LOCATION: 1..738
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT      48
75 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
76   1             5             10             15
78 AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG      96
79 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
80             20             25             30
82 GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA      144
83 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
84             35             40             45
86 CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA      192
87 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
88   50             55             60
90 TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA      240
91 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
92  65             70             75             80
94 GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC      288
95 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
96             85             90             95
98 ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG      336
99 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
100             100             105             110
102 TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT      384
103 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
104             115             120             125
106 TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG      432
107 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
108             130             135             140
110 TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT      480
111 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
112 145             150             155             160
114 ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA      528
115 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
116             165             170             175
118 ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG      576
119 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
120             180             185             190
122 TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT      624
123 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
124             195             200             205
126 TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC      672
127 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro

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128      210      215      220
130 TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA      720
131 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
132 225      230      235      240
134 GTT CGA GAT ATA GAT TGA GCGCCAGTTT TTGGAGTGTT ATGTATTTCC      768
135 Val Arg Asp Ile Asp *
136      245
138 TGGATGTTTG GAAACATTTT TTAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC      828
140 TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTGTAGAG      888
142 AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT      948
144 TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT      1008
146 ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCAATGTC CCCTTCGCAG      1068
148 CTGAAGTGGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCCT      1128
150 TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA      1188
152 TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAAATGTTT TCTTTGCAAA      1248
154 GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGTCTTGCT      1308
156 GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC      1368
158 CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCTTAATA TCAAAATGCAG      1428
160 TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTCAG ACTTGTCAAG CCTGTGCAAA      1488
162 AAAATTAATA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA      1548
164 TTTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC      1608
166 TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTCCAC AAGTGCCGCA      1668
168 AATTGTACCT TTTTGTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGTTT ATCAGCAAAA      1728
170 AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAAC ATTGCCCTTG      1788
172 AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC      1823
175 (2) INFORMATION FOR SEQ ID NO: 2:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 245 amino acids
179 (B) TYPE: amino acid
180 (D) TOPOLOGY: linear
182 (ii) MOLECULE TYPE: protein
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
186 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
187 1      5      10      15
189 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
190      20      25      30
192 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
193      35      40      45
195 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
196      50      55      60
198 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
199      65      70      75      80
201 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
202      85      90      95
204 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
205      100      105      110
207 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
208      115      120      125
210 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu

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Input Set : N:\Crf3\RULE60\10017910.txt

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```

211      130      135      140
213 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
214 145      150      155      160
216 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
217      165      170      175
219 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
220      180      185      190
222 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
223      195      200      205
225 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
226      210      215      220
228 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
229 225      230      235      240
231 Val Arg Asp Ile Asp
232      245
234 (2) INFORMATION FOR SEQ ID NO: 3:
236 (i) SEQUENCE CHARACTERISTICS:
237 (A) LENGTH: 2237 base pairs
238 (B) TYPE: nucleic acid
239 (C) STRANDEDNESS: double
240 (D) TOPOLOGY: linear
242 (ii) MOLECULE TYPE: cDNA
244 (iii) HYPOTHETICAL: NO
246 (vi) ORIGINAL SOURCE:
247 (A) ORGANISM: Mus musculus
249 (ix) FEATURE:
250 (A) NAME/KEY: CDS
251 (B) LOCATION: 142..1092
254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
256 CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCTGGGGCG GGGGCCGTGG      60
258 CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC      120
260 CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG      171
261 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
W--> 262      250      255
264 TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC      219
265 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
W--> 266      260      265      270
268 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA      267
269 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
W--> 270      275      280      285
272 CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG      315
273 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
W--> 274      290      295      300
276 GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG      363
277 Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
W--> 278 305      310      315      320
280 ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA      411
281 Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
W--> 282      325      330      335

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284 ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG      459
285 Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
W--> 286          340          345          350
288 AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT      507
289 Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
W--> 290          355          360          365
292 CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC      555
293 Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
W--> 294          370          375          380
296 TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC      603
297 Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
W--> 298 385          390          395          400
300 CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT      651
301 Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
W--> 302          405          410          415
304 GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG      699
305 Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
W--> 306          420          425          430
308 TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC      747
309 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
W--> 310          435          440          445
312 GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC      795
313 Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
W--> 314          450          455          460
316 ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT      843
317 Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
W--> 318 465          470          475          480
320 CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT      891
321 Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
W--> 322          485          490          495
324 TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT      939
325 Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
W--> 326          500          505          510
328 TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC      987
329 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
W--> 330          515          520          525
332 CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG      1035
333 Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
W--> 334          530          535          540
336 GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC      1083
337 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
W--> 338 545          550          555          560
340 ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT      1132
341 Ile Asp *
344 TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG      1192
346 GCCCAGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG      1252
348 TAAAGTCCAT AGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTA      1312
350 TGATTTCTTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA      1372
352 CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA      1432

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VERIFICATION SUMMARY

DATE: 02/15/2002

PATENT APPLICATION: US/10/017,910

TIME: 15:47:45

Input Set : N:\Crif3\RULE60\10017910.txt

Output Set: N:\CRF3\02152002\J017910.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3